

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 17, 2003, 07:20:40 ; Search time 13.4351 Seconds
(without alignments)
228.975 Million cell updates/sec

Title: US-09-787-082-5

Perfect score: 190

Sequence: 1 CKGKGAKCSRLMYDCTGSCRSKCTRNLPG 32

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 151 | 79.5 | 25 | 2 JH0700 | omega-conotoxin MV |
| 2 | 120 | 63.2 | 25 | 2 JH0701 | omega-conotoxin MV |
| 3 | 112.5 | 59.2 | 29 | 2 JH0699 | omega-conotoxin MV |
| 4 | 104 | 54.7 | 29 | 2 A58537 | omega-conotoxin MV |
| 5 | 97.5 | 51.3 | 26 | 2 C44379 | omega-conotoxin GV |
| 6 | 75.5 | 39.7 | 29 | 2 A43620 | omega-conotoxin GV |
| 7 | 75.5 | 39.7 | 29 | 2 B43620 | omega-conotoxin GV |
| 8 | 70 | 36.8 | 686 | 2 T25987 | hypothetical prote |
| 9 | 64 | 33.7 | 72 | 2 S39417 | metallothionein 10 |
| 10 | 61.5 | 32.4 | 610 | 2 JC7530 | vascular apoptosis |
| 11 | 60.5 | 31.8 | 66 | 2 S58086 | metallothionein 3 |
| 12 | 60.5 | 31.8 | 68 | 2 A46034 | metallothionein 3 |
| 13 | 60.5 | 31.8 | 68 | 2 I67866 | growth inhibitor |
| 14 | 59.5 | 31.3 | 751 | 2 F87789 | protein C34G6.2 i |
| 15 | 59 | 31.1 | 72 | 2 S39416 | metallothionein 10 |
| 16 | 58 | 30.5 | 27 | 2 S19619 | delta-conotoxin Tx |
| 17 | 58 | 30.5 | 78 | 2 S12513 | delta-conotoxin Tx |
| 18 | 57.5 | 30.3 | 78 | 1 TI2B1A | proteinase inhibit |
| 19 | 57.5 | 30.3 | 78 | 1 TI2B1B | proteinase inhibit |
| 20 | 57.5 | 30.3 | 1369 | 2 S70713 | protein-tyrosine k |
| 21 | 57 | 30.0 | 24 | 2 B44379 | omega-conotoxin SV |
| 22 | 57 | 30.0 | 72 | 2 S39419 | metallothionein 10 |
| 23 | 56.5 | 29.7 | 73 | 1 NTKN6G | omega-conotoxin GV |
| 24 | 56 | 29.5 | 318 | 2 T05569 | hypothetical prote |
| 25 | 56 | 29.5 | 1051 | 2 JC4091 | glycoprotein A - p |
| 26 | 56 | 29.5 | 2664 | 2 T28626 | variant-specific s |
| 27 | 55.5 | 28.2 | 79 | 1 TI2B2 | proteinase inhibit |
| 28 | 55 | 28.9 | 60 | 1 SMH01A | metallothionein 1A |
| 29 | 55 | 28.9 | 65 | 2 A38739 | metallothionein - |

30 55 28.9 68 2 B46034 metallothionein 3,
31 55 28.9 68 2 S44392 metallothionein 3
32 55 28.9 68 2 JC6521 metallothionein II
33 55 28.9 615 1 KFRU12 coagulation factor
34 55 28.9 1506 2 A96808 hypothetical prote
35 54 28.4 61 2 A27652 metallothionein 1A
36 54 28.4 61 2 S54332 metallothionein-2B
37 54 28.4 61 2 S54332 metallothionein-2D
38 54 28.4 61 2 S54333 metallothionein-2E
39 54 28.4 478 2 A43296 atropisin E (EC 3.
40 54 28.4 761 2 E64449 hypothetical prote
41 54 28.4 1589 2 C44766 defective chorion-
42 53.5 28.2 64 2 I56825 endogenous HIV-1 r
43 53.5 28.2 194 2 H64392 heterodisulfide re
44 53.5 28.2 491 2 S52920 disintegrin (EC 3.
45 53.5 28.2 544 2 S52477 disintegrin (EC 3.

ALIGNMENTS

RESULT 1

JH0700

omega-conotoxin MVIIA [validated] - cone shell (Conus magus)

C:Species: Conus magus (conus cone)

C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 15-Sep-2000

C:Accession: JH0700; C60133; A34115

R:Hillyard, D.R.; Monje, V.D.; Mintz, I.M.; Bean, B.P.; Nadasdi, L.; Ramachandran, J. Neuron 9, 69-77, 1992

A:Title: A new conus peptide ligand for mammalian presynaptic Ca2+ channels.

A:Reference number: JH0699; MUID:92337922; PMID:1352986

A:Accession: JH0700

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-25 <HIL>

R:Olivera, B.M.; Gray, W.R.; Zeikus, R.; McIntosh, J.M.; Varga, J.; Rivier, J.; de Sa

Science 230, 1338-1343, 1985

A:Title: Peptide neurotoxins from fish-hunting cone snails.

A:Reference number: A43620; MUID:86070213; PMID:4071055

A:Accession: C60133

A:Molecule type: protein

A:Residues: 1-25 <OLI>

R:Olivera, B.M.; Cruz, L.J.; de Santos, V.; LeCheminant, G.W.; Griffin, D.; Zeikus, R

Biochemistry 26, 2086-2090, 1987

A:Title: Neuronal calcium channel antagonists. Discrimination between calcium channel

A:Reference number: A34115; MUID:87299637; PMID:2441741

A:Contents: annotation

R:Nielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; Craik, D.J.

submitted to the Brookhaven Protein Data Bank, August 1996

A:Reference number: A67648; PDB:1MVI

A:Contents: annotation; conformation by (1)H-NMR, residues 1-25

R:Nielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; Craik, D.J.

J. Mol. Biol. 263, 297-310, 1996

A:Title: A consensus structure for omega-conotoxins with different selectivities for

A:Reference number: A58619; MUID:97070382; PMID:8913308

A:Contents: annotation; conformation by (1)H-NMR

R:Kohn, T.; Kim, J.I.; Kobayashi, K.; Koder, Y.; Maeda, T.; Sato, K.

submitted to the Brookhaven Protein Data Bank, April 1995

A:Reference number: A66296; PDB:1OMG

A:Contents: annotation; conformation by (1)H-NMR, residues 1-25

R:Kohn, T.; Kim, J.I.; Kobayashi, K.; Koder, Y.; Maeda, T.; Sato, K.

Biochemistry 34, 10256-10265, 1995

A:Title: Three-dimensional structure in solution of the calcium channel blocker omega

A:Reference number: A58627; MUID:95367555; PMID:7640281

A:Contents: annotation; conformation by (1)H-NMR

C:Superfamily: omega-conotoxin

C:Keywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel

F:1-16,8-20,15-25/Disulfide bonds: #status predicted

F:25/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 79.5%; Score 151; DB 2; Length 25;

Best Local Similarity 100.0%; Pred. No. 2.3e-10;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

C; Keywords: acetylcholine release inhibition; amidated carboxyl end; cal

Query Match 51.3%; Score 97.5; DB 2; Length 26;
Best Local Similarity 65.4%; Pred. No. 0.00018;
Matches 17; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 1 CKKGAKCSRLMYDCTGSC-RSGKC 25
|| || | : ||||| |||||
Db 1 CKLKGQSCRKTSYDCGSGCRSGKC 26

RESULT 6

A43620
omega-conotoxin GVIIA - cone shell (Conus geographus)
N:Alternate names: shaker peptide GVIIA
C:Species: Conus geographus (geography cone)
C:Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 23-May-1997
C:Accession: A43620
R:Oliviera, B.M.; Gray, W.R.; Zeikus, R.; McIntosh, J.M.; Varga, J.; Rivier, J.; de Santis
Science 230, 1338-1343, 1985
A:Title: Peptide neurotoxins from fish-hunting cone snails.
A:Reference number: A43620; MUID:86070213; PMID:4071055
A:Accession: A43620
A:Molecule type: protein
A:Residues: 1-29 <OLI>
C:Superfamily: omega-conotoxin
C:Keywords: acetylcholine release inhibition; calcium channel inhibitor; hydroxyproline;
F:1-16,8-19,15-26/Disulfide bonds: #status predicted
F:4,7/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 39.7%; Score 75.5; DB 2; Length 29;
Best Local Similarity 58.6%; Pred. No. 0.049;
Matches 17; Conservative 0; Mismatches 9; Indels 3; Gaps 2;

QY 1 CKKGAKCSRLMYDCTGSC--RSGKCTR 27
|| || || || || || || || || || || || ||
Db 1 CKSPGTPCSRGMRDCT-SCLYSNKCRR 28

RESULT 7

B43620
omega-conotoxin GVIIIB - cone shell (Conus geographus)
N:Alternate names: shaker peptide GVIIIB
C:Species: Conus geographus (geography cone)
C:Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 23-May-1997
C:Accession: B43620
R:Oliviera, B.M.; Gray, W.R.; Zeikus, R.; McIntosh, J.M.; Varga, J.; Rivier, J.; de Santis
Science 230, 1338-1343, 1985
A:Title: Peptide neurotoxins from fish-hunting cone snails.
A:Reference number: A43620; MUID:86070213; PMID:4071055
A:Accession: B43620
A:Molecule type: protein
A:Residues: 1-29 <OLI>
C:Superfamily: omega-conotoxin
C:Keywords: acetylcholine release inhibition; calcium channel inhibitor; hydroxyproline;
F:1-16,8-19,15-26/Disulfide bonds: #status predicted
F:4,7/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 39.7%; Score 75.5; DB 2; Length 29;
Best Local Similarity 58.6%; Pred. No. 0.049;
Matches 17; Conservative 0; Mismatches 9; Indels 3; Gaps 2;

QY 1 CKKGAKCSRLMYDCTGSC--RSGKCTR 27
|| || || || || || || || || || || || ||
Db 1 CKSPGTPCSRGMRDCT-SCLYSNKCRR 28

RESULT 8

T25987
hypothetical protein ZK154.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T25987
R:Connell, M.

submitted to the EMBL Data Library, September 1996
A:Description: The sequence of C. elegans cosmid ZK154.

A:Reference number: Z20119
A:Accession: T25987
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-686 <CON>
A:Cross-references: EMBL:U70844; PIDN:AAB09097.1; GSPDB:GN00028; CESP:ZK154.7
A:Experimental source: strain Bristol N2; clone ZK154
C:Genetics:
A:Gene: CESP:ZK154.7
A:Map position: X
A:Introns: 20/1; 49/1; 89/1; 155/3; 244/2; 282/3; 371/1; 419/3; 469/1; 521/2; 569/1;

Query Match 36.8%; Score 70; DB 2; Length 586;
Best Local Similarity 50.0%; Pred. No. 1.6;
Matches 14; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 5 GAKCSRLMYDCTGSCRGKCTRNLPG 32
||||| | : ||| : | |||
Db 482 GAKCSPLNHICCTPTCQFHNSTHVCLPG 509

RESULT 9

S39417
metallothionein 10-II - blue mussel
C:Species: Mytilus edulis (blue mussel)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
C:Accession: S39417
R:MacKay, E.A.; Overnell, J.; Dunbar, B.; Davidson, I.; Hunziker, P.E.; Kaegl, J.H.R.
Eur. J. Biochem. 218, 183-194, 1993
A:Title: Complete amino acid sequences of five dimeric and four monomeric forms of me
A:Reference number: S39416; MUID:94062828; PMID:8243463
A:Accession: S39417
A:Molecule type: protein
A:Residues: 1-72 <MAC>
C:Superfamily: metallothionein
C:Keywords: metal binding

Query Match 33.7%; Score 64; DB 2; Length 72;
Best Local Similarity 50.0%; Pred. No. 1.6;
Matches 14; Conservative 1; Mismatches 11; Indels 2; Gaps 2;

QY 1 CKKGAKCSRLMYDC-CTGSCRGK-CT 26
|| || || || || || || || || || || || ||
Db 31 CSGADCKCSGCKVVKCGSGCEGKGC 58

RESULT 10

JC7530
vascular apoptosis-inducing protein 1 - western diamondback rattlesnake
C:Species: Crotalus atrox (western diamondback rattlesnake)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 01-Mar-2002
C:Accession: JC7530; PC7105
R:Masuda, S.; Ohta, T.; Kaji, K.; Fox, J.W.; Hayashi, H.; Ataki, S.
Biochem. Biophys. Res. Commun. 278, 197-204, 2000
A:Title: cDNA cloning and characterization of vascular apoptosis-inducing protein 1.
A:Reference number: JC7530; MUID:20525424; PMID:11071872
A:Contents: Crude venom gland
A:Accession: JC7530
A:Molecule type: mRNA
A:Residues: 1-610 <NAS>
A:Cross-references: DDBJ:AB042840
A:Accession: PC7105
A:Molecule type: protein
A:Residues: 240-251;274-283;378-385;507-519 <MA2>
C:Comment: This protein, as a homodimeric protein, belongs to snake venom metallopro
a specific substrate, induces apoptosis in vascular endothelial cells.

C:Genetics:
A:Gene: vapl
C:Superfamily: mouse meltrin alpha; disintegrin homology
C:Keywords: apoptosis

A;Molecule type: protein
A;Residues: 1-72 <MAC>
C;Superfamily: metallothionein
C;Keywords: metal binding

Query Match 31.1%; Score 59; DB 2; Length 72;
Best Local Similarity 46.4%; Pred. NO. 5.8;
Matches 13; Conservative 1; Mismatches 12; Indels 2; Gaps 2;

QY 1 CKKGKAGCSRLMYDC-CTGSCRSRK-CT 26
| | | | | | | | | | | | | | | | | | | | | |
Db 31 CSGADCKCSGCKVVKCSGRCECGGCT 58

Search completed: March 17, 2003, 07:27:25
Job time : 15.4351 secs

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